Claims

1. A method for identifying phenotypes that vary in cell lines as a result of genetic variation, comprising:

(a) measuring one or more phenotypes in cell lines from one or more pedigrees; and

(b) testing whether the pattern of phenotype data in the cell lines conforms to the rules of Mendelian transmission,

wherein conformation of said phenotype data to the rules of Mendelian transmission is indicative that said phenotype varies in cell lines as a result of genetic variation.

2. A method for identifying phenotypes that vary in cell lines as a result of genetic variation, comprising:

(a) measuring one or more phenotypes in cell lines from one or more pedigrees; and

(b) testing whether the pattern of phenotype variation in the cell lines segregates in the pedigree so as to produce a LOD score of at least 2 with one or more loci, and wherein detection of a LOD score of at least 2 is indicative that said phenotype varies in cell lines as a result of genetic variation.

3. The method of claim 1, wherein the phenotype is the mRNA level of a selected gene.

4. The method of claim 2 where the LOD score is at least 3.

5. The method of any of claims 1 or 2, wherein the cell lines are derived from the CEPH pedigrees.

6. The method of any of claims 1 or 2, wherein the gene or genes responsible for the inter-cell line variation in phenotype are mapped to chromosomal loci by comparison of the pattern of segregation of the phenotype in the cell lines with the pattern of segregation of known mapped variances in the same cell lines.

7. The method of claim 4, wherein one or more candidate genes are evaluated by determining if their chromosomal position is one of the chromosomal positions (loci) that displays segregation with the phenotype.

8. The method of any of claims1 or 2, wherein at least 15 cell lines from related individuals are tested.

9. The method of any of claims 1 or 2, wherein the cells are subjected to a treatment before measuring the phenotype, the treatment selected from the group consisting of:

a. addition of a compound to the cells,

b. change in the nutritional environment of the cells, and

c. change in the physical environment of the cells.

10. A method for identifying mRNAs that vary in levels as a result of genetic variation, comprising:

a. measuring levels of one or more specific mRNAs in cell lines from one or more pedigrees; and

b. testing whether the mRNA levels of said one or more specific mRNAs in said cell lines conforms to the rules of Mendelian transmission,

wherein conformation of any of said mRNA levels to the rules of Mendelian transmission is indicative that said mRNA level varies in cell lines as a result of genetic variation.

11. The method of claim 10, wherein said cell lines are derived from one or more of the CEPH pedigrees.

12. The method of claim 10, wherein the gene or genes responsible for the intersubject variation in levels of specific mRNAs are mapped to chromosomal loci by comparison of the pattern of segregation of the mRNA levels in the cell lines with the pattern of segregation of variances that are already mapped to the human genome.

13. The method of claim 10, wherein at least 100 cell lines from related individuals are tested.

14. The method of claim 10, wherein said cells are subjected to a treatment before performing the RNA analysis, the treatment selected from the group consisting of:

a. addition of a compound to the cells,

b. change in the nutritional environment of the cells, and

c. change in the physical environment of the cells.

15. A method for the identification of phenotypes that vary among cell lines as a consequence of genetic variation, the method comprising:

a. Determining the genotype of a set of cell lines from unrelated subjects at candidate genes for the phenotypes of interest;

b. measuring the phenotype in the cell lines; and

c. Measuring whether genetic variation among the cell lines correlates with variation in the phenotype.

16. The method of claim 15 where at lest 20 cell lines are analyzed.